

OIPF

RAW SEQUENCE LISTING

DATE: 01/10/2002

PATENT APPLICATION: US/10/000,213

TIME: 15:56:00

Input Set : A:\RTS-0327 Sequence Listing.txt

Output Set: N:\CRF3\01102002\J000213.raw

ENTERED

3 <110> APPLICANT: Brenda F. Baker
 4 Mark P. Roach
 5 Kenneth Dobie
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF VITAMIN D NUCLEAR RECEPTOR
 EXPRESSION
 9 <130> FILE REFERENCE: RTS-0327
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/000,213
 C--> 11 <141> CURRENT FILING DATE: 2001-11-14
 11 <160> NUMBER OF SEQ ID NOS: 94
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 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 21 <223> OTHER INFORMATION: Antisense Oligonucleotide
 23 <400> SEQUENCE: 1
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 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 34 <223> OTHER INFORMATION: Antisense Oligonucleotide
 36 <400> SEQUENCE: 2
 37 atgcattctg cccccaagga 20
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 4604
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
 45 <220> FEATURE:
 47 <220> FEATURE:
 48 <221> NAME/KEY: CDS
 49 <222> LOCATION: (116)...(1399)
 51 <400> SEQUENCE: 3
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 53 acctcacaga agagcaccgc tgggtccac ttacctgcc cctgctcctt caggg atg 118
 54 Met
 55 1
 57 gag gca atg gcg gcc agc act tcc ctg cct gac cct gga gac ttt gac 166
 58 Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly Asp Phe Asp
 59 5 10 15
 61 cgg aac gtg ccc cgg atc tgt ggg gtg tgt gga gac cga gcc act ggc 214
 62 Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr Gly
 63 20 25 30
 65 ttt cac ttc aat gct cys Glu Gly Cys Lys Gly Phe Phe Arg 262
 66 35 40 45
 69 cga agc atg aag cgg aag gca cta ttc acc tgc ccc ttc aac ggg gac 310

VsrJ000213.htm

file:///C:

1/10/02

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70 Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly Asp
71 50 55 60 65
73 tgc cgc atc acc aag gac aac cga cgc cac tgc cag gcc tgc cgg ctc 358
74 Cys Arg Ile Thr Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg Leu
75 70 75 80
77 aaa cgc tgt gtg gac atc ggc atg atg aag gag ttc att ctg aca gat 406
78 Lys Arg Cys Val Asp Ile Gly Met Met Lys Glu Phe Ile Leu Thr Asp
79 85 90 95
81 gag gaa gtg cag agg aag cgg gag atg atc ctg aag cgg aag gag gag 454
82 Glu Glu Val Gln Arg Lys Arg Glu Met Ile Leu Lys Arg Lys Glu Glu
83 100 105 110
85 gag gcc ttg aag gac agt ctg cgg ccc aag ctg tct gag gag cag cag 502
86 Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu Glu Gln Gln
87 115 120 125
89 cgc atc att gcc ata ctg ctg gac gcc cac cat aag acc tac gac ccc 550
90 Arg Ile Ile Ala Ile Leu Asp Ala His His Lys Thr Tyr Asp Pro
91 130 135 140 145
93 acc tac tcc gac ttc tgc cag ttc cgg cct cca gtt cgt gtg aat gat 598
94 Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg Val Asn Asp
95 150 155 160
97 ggt gga ggg agc cat cct tcc agg ccc aac tcc aqa cac act ccc agc 646
98 Gly Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His Thr Pro Ser
99 165 170 175
101 ttc tct ggg gac tcc tcc tcc tcc tgc tca gat cac tgt atc acc tct 694
102 Phe Ser Gly Asp Ser Ser Ser Ser Cys Ser Asp His Cys Ile Thr Ser
103 180 185 190
105 tca gac atg atg gac tcg tcc agc ttc tcc aat ctg gat ctg agt gaa 742
106 Ser Asp Met Met Asp Ser Ser Ser Phe Ser Asn Leu Asp Leu Ser Glu
107 195 200 205
109 gaa gat tca gat gac cct tct gtg acc cta gag ctg tcc cag ctc tcc 790
110 Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser Gln Leu Ser
111 210 215 220 225
113 atg ctg ccc cac ctg gct gac ctg gtc agt tac agc atc caa aag gtc 838
114 Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile Gln Lys Val
115 230 235 240
117 att ggc ttt gct aag atg ata cca gga ttc aga gac ctc acc tct gag 886
118 Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu Thr Ser Glu
119 245 250 255
121 gac cag atc gta ctg ctg aag tca agt gcc att gag gtc atc atg ttg 934
122 Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val Ile Met Leu
123 260 265 270
125 cgc tcc aat gag tcc ttc acc atg gac gac atg tcc tgg acc tgt ggc 982
126 Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp Thr Cys Gly
127 275 280 285
129 aac caa gac tac aag tac cgc gtc agt gac gtg acc aaa gcc gga cac 1030
130 Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys Ala Gly His
131 290 295 300 305
133 agc ctg gag ctg att gag ccc ctc atc aag ttc cag gtg gga ctg aag 1078
134 Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val Gly Leu Lys

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135          310          315          320
137 aag ctg aac ttg cat gag gag gag cat gtc ctg ctc atg gcc atc tgc      1126
138 Lys Leu Asn Leu His Glu Glu Glu His Val Leu Leu Met Ala Ile Cys
139          325          330          335
141 atc gtc tcc cca gat cgt cct ggg gtg cag gac gcc gcg ctg att gag      1174
142 Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala Leu Ile Glu
143          340          345          350
145 gcc atc cag gac cgc ctg tcc aac aca ctg cag acg tac atc cgc tgc      1222
146 Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr Ile Arg Cys
147          355          360          365
149 cgc cac ccg ccc ccg ggc agc cac ctg ctc tat gcc aag atg atc cag      1270
150 Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys Met Ile Gln
151 370          375          380          385
153 aag cta gcc gac ctg cgc agc ctc aat gag gag cac tcc aag cag tac      1318
154 Lys Leu Ala Asp Arg Ser Leu Asn Glu Glu His Ser Lys Gln Tyr
155          390          395          400
157 cgc tgc ctc tcc ttc cag cct gag tgc agc atg aag cta acg ccc ctt      1366
158 Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu Thr Pro Leu
159          405          410          415
161 gtg ctc gaa gtg ttt ggc aat gag atc tcc tga ctaggacagc ctgtgcggtg      1419
162 Val Leu Glu Val Phe Gly Asn Glu Ile Ser
163          420          425
165 cctgggtggg gctgctctc cagggccacg tgccaggccc ggggctggcg gctactcagc      1479
166 agccctcctc accgctctgg ggttcagccc ctccctctgcc acctccccta tccaccacgc      1539
167 ccattctctc tctgtccaa cctaaccctt ttcttgctgg cttttccccc gtcccttgag      1599
168 acctcagcca tgaggagttg ctggttgttt gacaaagaaa cccaagtggg ggcagagggc      1659
169 agaggttggg ggcaggcctt gccagagatg gctccaccg ctgcctaagt ggcgtctgac      1719
170 tgatgttgag ggaacagaca ggagaaatgc atccattcct cagggacaga gacacctgca      1779
171 cctcccccca ctgcaggccc cgttgttcca gcgcctagt gggctccct ctctgcctt      1839
172 actcacgata aataatcggc ccacagctcc caccaccacc ccttcagtgc ccaccaacat      1899
173 ccattgccc tggttatatt ctacggggca gtagctgtgg tgagggtgggt tttcttccca      1959
174 tcactggagc accaggcacg aaccacactg ctgagagacc caaggaggaa aaacagacaa      2019
175 aaacagcctc acagaagaat atgacagctg tccctgtcac caagctcaca gttcctcgcc      2079
176 ctgggtctaa ggggttggtt gaggtggaag cctccttcc acggatccat gtagcaggac      2139
177 tgaattgtcc ccagtttgcg gaaaagcacc tgccgacctc gtccctcccc tgccagtgcc      2199
178 ttacctcctg cccaggagag ccagccctcc ctgtcctcct cggatcaccg agagtagccg      2259
179 agagcctgct cccccacccc ctcccagggg gagagggtct ggagaagcag tgagccgcat      2319
180 cttctccatc tggcagggtg ggatggagga gaagaatttt cagaccccag cggctgagtc      2379
181 atgatctccc tgccgcctca atgtggttgc aaggccgctg ttcaccacag ggctaagagc      2439
182 taggtgccc caccacagag tgtgggaagg gagagcgggg cagtctcggg tggctagtca      2499
183 gagagagtgt ttgggggttc cgtgatgtag ggtaagggtc cttcttatc tcactccacc      2559
184 acccaaaagt caaaagggtc ctgtgagga ggggcggagt gatacaactt caagtgcagt      2619
185 ctctctgcag gtcgagccca gccagctgg tgggaagcgt ctgtccgttt actccaagg      2679
186 gggctcttgt gagagtgagc tgtaggtgtg cgggaccggt acagaaaggc gttcttcgag      2739
187 gtggatcaca gaggcttctt cagatcaatg cttgagtttg gaatcgcccg cattccctga      2799
188 gtcaccagga atgttaaagt cagtgggaac gtgactgcc caactcctgg aagctgtgtc      2859
189 cttgcacctg catccgtagt tccctgaaaa cccagagagg aatcagactt cacactgcaa      2919
190 gagccttggt gtccacctgg ccccatgtct ctccagaattc ttcaggtgga aaaacatctg      2979
191 aaagccacgt tccttactgc agaatagcat atatatcgt taatcttaaa tttattagat      3039

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192 atgagttggtt ttcagactca gactccattt gtattatagt ctaatatata gggtagcagg 3099
193 taccactgat ttggagatat ttatgggggg agaacttaca ttgtgaaact tctgtacatt 3159
194 aattattatt gctgttggtt ttttacaagg gtctagggag agacccttgt ttgattttag 3219
195 ctgcagaact gtatttggtc agcttgcctc tcagtgaggag aaaaacactt gtaagttgct 3279
196 aaacgagtca atccctcat tcaggaaaac tgacagagga gggcgtgact cacccaagcc 3339
197 atatataact agctagaagt gggccaggac aggcggggcg cggtggtcga cgcctgtaat 3399
198 cccagcagtt tgggaggtcg aggtaggtgg atcacctgag gtcgggagtt cgagaccaac 3459
199 ctgaccaaca tggagaaacc ctgtctctat taaaaatata aaaaaaaaaa aaaaaaaaaa 3519
200 tagccgggca tggtgggcga agcctgtaat cccagctact caggaggctg aggcagaaga 3579
201 attgaaccca ggaagtggag gttgcagtga gctgagatcg tgccttact ctccaacctg 3639
202 gacaacaaga gcaaaactcc gtcttagaag tggaccagga caggaccaga ttttgagtc 3699
203 atggctcggg gtccctttca ctacaccatg tttgagctca gacccccact ctcatcccc 3759
204 aggtggctga cccagtcctt gggggaagcc ctggatttca gaaagagcca agtctggatc 3819
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207 ctgctgggct ctccacctca ggccttggat aatgctgttg cctcatctat aacatgcatt 3999
208 tgtctttgta atgtcaccac ctcccagct ctccctctgg cctgcttct tcggggaact 4059
209 cctgaaatat cagttactca gccctgggce ccaccaccta ggcactcct ccaaaggaag 4119
210 tctaggagct gggaggaaaa gaaaagaggg gaaaatgagt ttttatggg ctgaacgggg 4179
211 agaaaaggct atcatcgatt ctactttaga atgagagtgt gaaatagaca tttgtaaatg 4239
212 taaaactttt aaggtatata attataactg aaggagaagg tgcccaaaa tgcaagattt 4299
213 tccacaagat tcccagagac aggaaaatcc tctggctggc taactggaag catgtaggag 4359
214 aatccaagcg aggtcaacag agaagggcag aatgtgtggc agatttagtg aaagctagag 4419
215 atatggcagc gaaaggatgt aaacagtgcc tgctgaatga tttccaaaga gaaaaaaagt 4479
216 ttgccagaag tttgtcaagt caaccaatgt agaaagcttt gcttatggta ataaaaatgg 4539
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218 aaacc 4604

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221 <211> LENGTH: 20

222 <212> TYPE: DNA

223 <213> ORGANISM: Artificial Sequence

225 <220> FEATURE:

227 <223> OTHER INFORMATION: PCR Primer

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236 <213> ORGANISM: Artificial Sequence

238 <220> FEATURE:

240 <223> OTHER INFORMATION: PCR Primer

242 <400> SEQUENCE: 5

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19

246 <210> SEQ ID NO: 6

247 <211> LENGTH: 27

248 <212> TYPE: DNA

249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

253 <223> OTHER INFORMATION: PCR Probe

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262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
266 <223> OTHER INFORMATION: PCR Primer
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273 <211> LENGTH: 20
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
279 <223> OTHER INFORMATION: PCR Primer
281 <400> SEQUENCE: 8
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285 <210> SEQ ID NO: 9
286 <211> LENGTH: 20
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
292 <223> OTHER INFORMATION: PCR Probe
294 <400> SEQUENCE: 9
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298 <210> SEQ ID NO: 10
299 <211> LENGTH: 77
300 <212> TYPE: DNA
301 <213> ORGANISM: Homo sapiens
303 <220> FEATURE:
306 <400> SEQUENCE: 10
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309 cccgccggcc ggaccag 77
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313 <211> LENGTH: 121
314 <212> TYPE: DNA
315 <213> ORGANISM: Homo sapiens
317 <220> FEATURE:
320 <400> SEQUENCE: 11
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323 tggcaggccc cgtgctcatt gctttgcttg cctccctcaa tctcatagc ttctctttgg 120
325 g 121
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329 <211> LENGTH: 45000
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <400> SEQUENCE: 12
334 ctgagcacca ggaaaggagc ctgaggaatc aataaggcca gaggaggaac cctgcagagc 60

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/000,213

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Input Set : A:\RTS-0327 Sequence Listing.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date